

9.5 →  
7.5 →  
4.4 →  
2.4 →  
1.4 →  
0.24 →

Non-fruited  
L S R  
Fruited  
L S R  
G G/R R/G R B

0.89

pRIB 1

2/11

1 CAGCATTCCA AGAGGAAAAA AAACATGATC AAGAAGTAAT TACTACAAAA  
 51 GAGGAAGCTG TAGTAGTAAC TGCACCACCA CCATCAGAAA CAGCAGAGCC  
 101 AGCTGCAGCT GTTGTGCGG AGGAAGAGAC AACAAAGGAG CAAGAAGAGC  
 151 CGCCAGCAGT ATCGGCCGAG GAACCTGTGG CCCCAGCTGA AGTAGAGACA  
 201 AAGGTGGAAG TTACAGAAGA ACCACCAAAA GTTGAGGAGA AACCAGCAGA  
 251 AGTAGAGGAG GCTCCAAAGG AAACAGTAGA AACAGAACCA GCTGTTGAGA  
 301 AGACCATCAA GGAGGAAACT GTAGAGGACT CTGTCGTGGC ACCTGCTCCC  
 351 GAACCGGAAG CCGAAGTCCC AAAAGAGAAG GTAATTGCTA CTACTGAAAC  
 401 TACTGAGGAA GAAGAAAAAG TGGCAGTTGA AGAAGTTGAA GTGAAAGTTG  
 451 AAACAGAGGA GGGAGAAGTT ACTGAGGAGA AGACTGAGTA AAATAAGTTG  
 501 TACAACTATT TTATGCACGC CTTATTTTCT CAATTGGAAG TTTATAATGT  
 551 AGTGGGCTTT TGGTAATATT TGGGGGTTTA ATAAGTGTT TAAGTGGGTT  
 601 AAGGCTTTTT TGGAATTTAG ATATTTGGGT AAAGGCCTAC TTGAACAAAA  
 651 CATAGAAATT TGGCACACAT GGGTAAAAGT CAACTTTTGT TGAGGATGTT  
 701 TTCTTGTTGG TTAAATGTGT GTGCCAAGTA GTAGAATGTG GTGGTTGTAA  
 751 TGTAAGTTCT CAAGTAGGGT TTATGAGTCC TAGTATTATG CTTGATTGTA  
 801 TGTGATATG AAAATGGGGG TATGTTGGCT TTGAATAAAA GTTTTTAATT  
 851 TTATAAAAAA AAAAAAAAAA AAAAAAAAAA AA

Figure 3

1 AFQEEKKHDQ EVITTKEEAV VVTAPPPSET AEPAAAVVAE EETTKEQEEP  
51 PAVSAEEPVA PAEVETKVEV TEEPPKVEEK PAVEEAPKE TVETEPAVEK  
101 TIKEETVEDS VVAPAPEPEA EVPKEKVIAT TETTEEEKV AVVEVEVKVE  
151 TEEGEVTEEK TE

Figure 4

1 AAACAACAACTTTTTTCATCAATCTTCTTTCTTTAATCATCACCATGTCGAGCTGCGGAA 60  
 T T N F F I N L L S L I I T M S S C G N  
 61 ACTGCGACTGTGCCGACAAGACCAACTGCCCAAAGAAGGGAAACAGCTACGGCTTTGACA 120  
 C D C A D K T N C P K K G N S Y G F D I  
 121 TCATTGAGACCCAGAAGAGCTACGATGACGTCGTGGTGATGGATGTTTCAGGCAGCTGAGA 180  
 I E T Q K S Y D D V V V M D V Q A A E N  
 181 ATGATGGCAAGTGCAAGTGCGGCCCCGAGCTGCAGTTGTGTGGGCTGCAGCTGTGGTCATT 240  
 D G K C K C G P S C S C V G C S C G H \*  
 241 AAGTTAAACACAACATTATCATGTTATAGTGAATAATGATGTGTGTGATGAATATAGGTG 300  
 301 AAAAATCTGTGGTGTGATAAAAACCGTTGGTGAATAAATAGGTGTATATTTTCGTGTGCAC 360  
 361 CTTCTACGAGTACTTGTGCTTGTGGGTGAAAGAAATATGCACCTAAGTGTGAGTTGTTT 420  
 421 TCCGTGTTTTTCGCCGTGTCCCTTGTAATGGTCATGTTTGTGTTTTCTTGTGGTTAAATT 480  
 481 AAATGAAC TAGTAATGTTATGTAAAAA 519

Figure 5





1 CCGTTCAATCGCTGGATCAATCGAGCATATGGCGATGTATCCGGTTGATACGCTTAAAAAC 60  
G S I A G S I E H M A M Y P V D T L K T

61 TCGCATACAGGCTATTGGGTCATGTTCCGGCTCAATCCGCCGGTCTCCGACAAGCCCTTGG 120  
R I Q A I G S C S A Q S A G L R Q A L G

121 GTCGATACTGAAAGTTGAAGGTCCCGCCGGACTTTACCGTGCGATTGGTGCAATGGGTCT 180  
S I L K V E G P A G L Y R G I G A M G L

181 CGGTGCAGGACCAGCTCACGCAGTGTATTTCTCCGTTTACGAGATGTGTAAGGAGACTTT 240  
G A G P A H A V Y F S V Y E M C K E T F

241 TTCTCATGGTGATCCGAGCAATTCCGGTGCGCACGCCGTTTCGGGGGTGTTGCGGACGGT 300  
S H G D P S N S G A H A V S G V F A T V

301 GGCAAGCGACGCGGTGATTACGCCGATGGATGTGGTGAAACAGAGGTTGCAGTTGCAGAG 360  
A S D A V I T P M D V V K Q R L Q L Q S

361 CAGTCCGTACAAGGGTGTGTTGATTGCGTGAGGAGGGTGTGTTGGTAGAAGAAGGGATTGG 420  
S P Y K G V V D C V R R V L V E E G I G

421 CGCATTTTACGCATCTTATCGAACAACGTGGTTCATGAATGCCCCGTTTACGGCCGTTCA 480  
A F Y A S Y R T T V V M N A P F T A V H

481 CTTGCCACATATGAAGCCACGAAGAAAGGGTGTGTTGGAGGTGTCGCCGGAGACTGCCAA 540  
F A T Y E A T K K G L L E V S P E T A N

541 CGATGAGAATTTGTTAGTGCGATGCTACTGCTGGTGCTGCTGCTGGAGCTTTGGCTGCAGT 600  
D E N L L V H A T A G A A A G A L A A V

601 AGTAACCACTCCACTAGATGTTGTCAA<sup>3</sup>AACTCAGTTGCAGTGCCAAGGTGTTTGCGGATG 660  
V T T P L D V V K T Q L Q C Q G V C G C

661 CGACAGATTTTCTAGCAGTTCGATTTCAGGATGTTATAGGAAGCATAGTGAAGAAAAATGG 720  
D R F S S S S I Q D V I G S I V K K N G

721 ATATGTCGGGTTAATGAGGGGGTGGATTCCCAGAATGCTATTTTCATGCTCCTGCTGCAGC 780  
Y V G L M R G W I P R M L F H A P A A A

781 AATCTGCTGGTCTACTTATGAAGCCTCCAAAACATTCTTTCAA<sup>3</sup>AACTCAATGAGAGCAA 840  
I C W S T Y E A S K T F F Q K L N E S N

841 TAGCAACAGCTCAGTTACCTAAGATTTTCATATGTTTTGTTGCTCTACTAGGCTTATCCA 900  
S N S S V T \*

901 AAATCATGTCGATTGGT<sup>3</sup>TTCACTTCACCACAGTTGCCATGAACAAC<sup>3</sup>TCAAAGCATCGAAT 960  
961 TTTCATGTATATTATGCAATCTAGATGCTTCTTGATATTTATTTTATTTTCTTTTCTTTT 1020  
1021 CAACTTTTGTAAATTAGAATTAGCTACTATGGTTATGGCATGGAGTGTTTATAATTGCTA 1080  
1081 ATATCATCGTATAAGCAATGCTATTGAGAAATTGTTGGTGAAGGTTAGAGTAATGTTAT 1140  
1141 TTGCACAATCCACTTACATAGACCGCGGGACTCATT<sup>3</sup>TAAAA<sup>3</sup>AAAAAAAAAAAAAAAA 1195

Figure 8



TTCTCTCTCT

1 GAGCTTATAT TGAAGTATGA AATTTTCANA TTACTGTATA TGTAACTCTC AACAAATACA AGCTTTTGTAT CATATTAATTC GAAACCAACA CACAATAAT

101 ATGAATTTCT TTGACATCTTT GTCTCTGTAC CAAATATGCG ACACCACAAA AATTTCTTTT TGTATATAT TCTTTTTTTA TTTTTTAAAC GTTTTGGTAT

201 TCAACATCA TATAAGTAAAG GGGGAATATTT ATTGGGACTC CTCCAAAAC TTATGACATT GTGATTACAC ATTGMAAGA CAGAAGTTTT TGATGAAGTG

301 CCAATATCAA TCTTTTCTTA ATTGCTTCAT AAAGGCTGT TTTGTAATTA AAGAAAGAT AAGGAATTT AGCAAGAAGT GCATTATTGG GACTGGTATA

401 TATGACAAAG ATCTGACTTG CCAAGAAAG AAAGTGGGTC CTGAGTCAGG TGTGTCCCAT CTGTCAATAT TCTTCAAAAG AGAGTCCACC ATCTCATAGA

501 TGAGATTTAG AAGTGTGTTT CCACAAABA ATATGACACA ACCATCCAT GAACCAATAA AACATGACA GGTCACTATT TCTTTCTATT TTTTCTCTC

601 AAGATATATA TACTATTAG TGTCTTTTAA ACCGGCTTAA CTTTGCATTT CTTGTCAATT GGTGACTTTT TATTGCCCAA TTGTGGCTTG AAGGAATAA

701 AAAGGAAGT CTTTTCTTGG ACCCATATG GAGCAATTT CAATGAGGA GATAGAGAGG AGGATGGAG ATTGGGTGG AGAATTGATA CGGATCTTCT

801 TTAATTGGTA TATGTAAATC ACTCAGAAAC ACATATACCA TATATGATC AATGTCATG TCACAGAAA CGTAACCTAC GNACACATTT CGTAACATGC

901 ATGCACCAAT CATACATTAT AACATAGTGT TACGACATA AAGATCTTT AGTCTAGA GCATTAGTC GTACACAGAA CAAAACCTG GATTTCCCAAC

1001 CTAAGAAGG GTATATCTTT TATTCATATA TCTACTTTTG ATATGACCTA AACCTTGTCT CACCCACAT GTTCAGTAGG ATCGATAATT GTTTGACTTG

1101 TGTGGGATGA GAAATGTAT GAGACTGGCC ATTAGTTTAA GCCGGATGT ATTGGGTAT ATTGATGACA ATATAGATA TATAAACTT GAACAAACA

1201 ATTCTTCAC AATTAATCT ACAAGATAT CTCTCTTCAG ATGATAACT AATGATAGA AATCTCTTG AGTACCCCA ATATTTTAA ATCTCCAGCA

1301 AATACATGA TTCTTTTCT TCGAGCGNA ATTCTTCTCT TCCAAACCC TTAACAATG TAAATTCGT TAGTAGATT AATTTGAAA TGNATACACA

1401 AGAGTGAATA AAGTCAATG TCACCTACTT ACCCACTGC ACAAAACACA CAGACACA TCCAAAGTA GTAGTATGAT TACACACATT TGAANAATG

1501 ACCTCCATTA TTTAGCCAC CTCTCTTGA AAGAGNTTA CAAGAAAT ACTCTATCA TTATATAA ATATAGTA TAACCTCATC TCCATCCAC

1601 ACCATATAT TTACATTAT GCCAAACATG CTAAGACTT CTTGTATTCA GTGAAATGT GGTGTCAAT CCCAGATTC TTCTGTGCC CTCTCTCTCT

1701 CTCTCTCTCT CTCTCTCTCT CTCTCTCTCT TCCTCTCTCT ATCAACTTGA GGGCTTTAGG ACCTCTATAT AAACCTCTCT CAATTGATCA TCTCTGC

← Putative promoter sequence

Figure 9

1	GATCTTATATTAGGAGTGCAAAAGTTTCAAATTACCTGATATGTAACCTCTCAACAAATATCA	60
61	AGCTTTTGTATCATATAAATCGAAACCAACACACAATAATTATGAATTTCTTTGACTCTTT	120
121	GTCTCTGTACCAAAATACGCACACCACAAAAAATCTTTTTGTATTATATTCTGTTTTTTA	180
181	TTTTTTTAAACGTTTTGGTATTCAAACATCATATAAGTAAGGGGGAATATTATTCTGGACTC	240
241	CTCCAAAACTTATGACATTGTGATTACACATTTGAATGACAGAAGTTTTTGATGAAGTG	300
301	CCAATATCAATCTTTTCTTAATTGCTTCATAAAGGGTGTTTTTGTAAATAAAAGAAAGAT	360
361	AAGGAAATTTAGCAAGAAGTGCAATTATTGGGACTGGTATATATGACAAGGATCTGACGTG	420
421	GCAAAGAAAGAAAGTGGGTCTGAGTCAGGTGTGTCCCATCTGTCAATATTCTTCAAAG	480
481	AGAGTCCACCATCTCATAGATGAGATTTAGAAAGTGGTTTTCCACAAAAAATATGACACA	540
541	ACCCATCCATGAACCAATAAAAAACATGACAGGTATCATTTTCTTTCTATTTTTTTCTCTC	600
601	AAGATAATAATACCTATTAGTGTCTTTAACACCGGCCTAACTTTGCATTTCTTGTCAATT	660
661	GGTGACTTTTTTATTGCCCCAATTGTGGCTTGAAGGAAATAAAAAGGAAAGTCTTTTTCTTG	720
721	AACCCATATGGAAGCAATTTCAATGAGAGAGATAGAGAGGAGGGATGGAGATTGGGGTGG	780
781	AGAATTGATACGGATCTTCTTTAATTGGTATATGTAAATCACTCAGAAACACGTATACCA	840
841	TATATGCATCAATGTCAATGTCACAGAAAACGTAACCTCAGAACACATTTTCGTAACATGC	900
901	ATGCACCAATCATACATTATAACATAGTGTTACGACAATAAAAAGATCTTTAGTCGTAAGA	960
961	GCATTAGCTCGTGACAAGAACAAAAACGTGGATTCCCAACCTAAAAGAGGGTATATCTTT	1020
1021	TATTATATATCTACTTTTTGATATGACCTAAACCTTGTGTCAACCCACAATGTTTCAGTACG	1080
1081	ATCGATAATTGTTTGACTTGTGTGGGATGAGAAAAATGATAGAGATCGCCATTAGTTTTA	1140
1141	CGCGGATGTGATTTGGGTATATTGATGACAAATATAAGATATATAAACTTGAACAAAAAC	1200
1201	ATTTCTCAACAAATTAAACTACAAGATAATCTCCCTTCAGATGATAAACTAAATGGTAGA	1260
1261	ATATCCGTTGAGTACCCCCAATAATTTAAAAATCTCCAGCAAATACTGTGATTCCTTTTCT	1320
1321	TCGAAGCGAAATTCCTTCTTCCAAACACCTTAACAAATGTAAATTCGTTAGTAAGATT	1380
1381	AAATTTGAAATGATAACACAAGAGTGAATAAAGGTCATGGTCACCTACTTACCCAACTGC	1440
1441	ACAAAACACACAAGCACACATCCAAAAGTAGTAGTATGATTACACACATTTGAAAAAATG	1500
1501	ACCTCCATTATTTTAGCCACCTCTCTTGTAAAAAAGATTACAAACAAATTACTCCTATCA	1560
1561	TTATTATAAAAAATAGTAGCATAACCTCATCTCCAATCCACACCATATATTTTACATTATT	1620
1621	GCCAAACATGCTAAAAGCTTCTTGATTTCAGTGAAAATGTGGTGTCAAATCCCAAGATT	1680
1681	TTCAATGTGCCCT	1740
1741	ATCAACTTGAGGGCTTTAGGACCTCTATATAAACTCTCTCAATTGATCATCTCTGTCATC	1800
1801	ACACTCTCAAGCATTCTTTCTCTCTACTTTCTTTTAGGTCAACTACACTTCCCTTTGAGT	1860
1861	TTCCAATGGCCACTGTTGAGGTAAATCAAGTGATATATACATAAAATTTTATTGAAAGAT	1920
M A T V E		
1921	GATTGATTCAAAGAGAACCCTTTTGTGTTTTCTTTAATAAGATCCATGTATATGAAGTTT	1980
1981	TAATGTTTCATGTTTTTTTTATTTTTTGTAAATTTTTTTTTTAATTTAGGCATTTTGTCAAT	2040
2041	ATCCCATTTGTGAAAAGATCTGTTTTCTTTGGAAGAGATTAGAATTCGTTTCGTGTCGA	2100
2101	TTCATCATGAAAATCAATCTGGGTCTAGCTTTAATTGTGCTGATCTTGACCGGACTGTTA	2160
2161	GATGATTCGTTTTATATGTAGGCCCAATAGAGAGTGATAGTATCCCGAAATAATACAAA	2220
2221	TCCGAGCAAACATATAATCCTCAATAGTAACTTTGTAATCTCTAAATAATCAAAAAATAAT	2280
2281	GCTTATTGGGGTGATTGGTGTGTTTGATGCAGGTGTGATCAGCGCAGACAGCATCTCAAG	2340
V V S A Q T A F Q E		
2341	AGGAAAAAAAACATGATCAAGAAGTAATTACTACAAAAGAGGAAGCTGTAGTAGTAACTG	2400
E K K H D Q E V I T T K E E A V V V T A		
2401	CACCACCACCATCAGAAACAGCAGAGCCAGCTGCAGCTGTTGTTGCCGAGGAAGAGACAA	2460
P P P S E T A E S A A A V V A E E E T T		
2461	CAAAGGAGCAAGAAGAGCCGCCAGCAGTATCGGCCGAGGAACCTGTGGCCCCAGCTGAAG	2520
K E Q E E P P A V S A E E P V A P A E V		
2521	TAGAGCAAAGGTGGAAGTTACAGAAGAACCACCAAAAGTTGAGGAGAAACCAGCAGAAG	2580
E T K V E V T E E P P K V E E K P A E V		
2581	TAGAGGAGGCTCCAAAGGAAACAGTAGAAACGAAACCAAGCTGTTGAGAAGACCATCAAGG	2640
E E A P K E T V E T E S A V E K T I K E		

Figure 10 a

2641 AGGAAACTGTAGAGGACTCTGTCGTGGCACCTGCTCCCGAACCGGAAGCCGAAGTCCCAA 2700  
       E T V E D S V V A P A P E P E A E V P K  
 2701 AAGAGAAGGTAATTGCTACTACTGAACTACTGAGGAAGAAGAAAAAGTGGCAGTTGAAG 2760  
       E K V I A T T E T T E E E E K V A V E E  
 2761 AAGTTGAAGTGAAAGTTGAAACAGAGGAGGGAGAAGTTACTGAGGAGAAGACTGAGTAAA 2820  
       V E V K V E T E E G E V T E E K T E \*  
 2821 ATAAGTTGTACAACACTATTTTATGCACGCCTTATTTTCTCAATTGGAAGTTTATAATGTAG 2880  
 2881 TGGGCTTTTGGTAATATTTGGGGGTTTAAATAAGTGGTTTAAAGTGGGTAAAGGCTTTTTTG 2940  
 2941 GAATTTAGATATTTGGGTAAAGGCCTACTTGAACAAAACATAGAAATTTGGCACACATGG 3000  
 3001 GTAAAAGTCAAACCTTTGTTGAGGATGTTTTCTTGTGTTAAATGTGTGTGCCAAGTAGT 3060  
 3061 AGAATGTGGTGGTTGTAATGTAAGTTCTCAAGTAGGGTTTATGAGTCCTAGTATTATGCT 3120  
 3121 TGATTGTATGTTGATATGAAAATGGGGGTATGTTGGCTTTGAATAAAAGTTTTTAATTTT 3180  
 3181 ATATAATAAGTGTATTTTTGTTTAAATATCATTCTTTTCATTCTCTCGGATCAACTACTGAT 3240  
 3241 CATCGCCTTGGTAAGCTATTGCCTCACCAACTAGCTAATCGAACGCGAGCCC 3292

Figure 10b